Evolutionary and population dynamics of infectious disease organisms with their natural vectors and hosts can be complex, but these complexities are often magnified when a native host encounters novel vectors and pathogens through introduction. The Hawaiian avifauna and introduced avian malaria is considered to be a classic case of an introduced parasite having extreme impacts on the fitness of immunologically naive native species. Genetic analyses of the *Culex quinquefasciatus* vector and avian malarial parasite (*Plasmodium relictum*) in Hawaii reveal a single genetic (Hawaii) strain of parasite, and a recent conversion from a New World to mostly an Old World (Australopacific) genotype of mosquito. The worldwide distributions of the Hawaiian malarial strain and the Australopacific *Culex* genotype suggest an interaction between the two. DNA analysis of museum specimens suggests a relatively late arrival for both to the islands (mid 1900s). The implications for the evolution of virulence of the parasite and for evolutionary dynamics of invasive or introduced vectors and pathogens, and their native hosts, will be discussed, along with suggestions for solutions to the major negative impacts this parasite currently has on native Hawaiian bird populations.